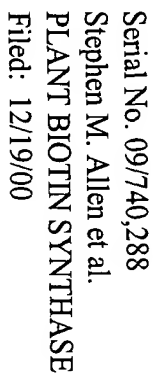


SID18	TTTTPS	-----	AVSP	SAAAPFRPALLAE	----	PAMLLLLARSLRSRVSPFASAVSAAPFSSVSAAAAEAERAVRDGPRNDWTRP				
SID20	MA	-----			-----	MLLARNLRSRLRPPLAA	AAAFSS	AAAEARAIRDGPRNDWSRP		
SID22	MA	-----			-----	MLLARNLRSRLRPPLAA	AAAFSS	AAAEARAIRDGPRNDWSRP		
SID24	MA	-----			-----	MLLARNLRSRLRPPLAA	AAAFSS	AAAEARAIRDGPRNDWSRP		
SID26		-----			-----	LRPLIFIS	TFSSSSSSSSAAAVQAERTIKEGPRNDWSRD			
SID28	TKPNPKHKYRCCLLSLSCLYSQISHSFVSLPNFEFESKNMFLARPIFRA	----	PSLWALHSSYAYSSASAAAIQAERAIKEGPRNDWSRD							
SID32	T	-----			-----					
1705463		-----			-----	MLVRSVFRSQ	LRPSV	SG	GLQSACYSLSAASAEARTIREGPRNDWSRD	
SID30	MAT	-----			-----	LRTSLRSLLILRSNTPKLAPIS	SSVRLQVQKS RNYGTVSSVPQATETTS	STPSKDVYQ	EALNATE	PRSNWTRP
2995363	M	-----			-----	FT	RTIRQ	IRSSALSIV		RNNWTRP
3321725	M	-----			-----	MSTIYRHLSTA	RPALTKYATNAA	VKSTTASSEASTIGALIOVALSL		DEPSHSWTKS

SID18 EIQAIYDPSPLDLLFHGAQVHRNVHKFREVOQCTLLSIKTGCCSEDCSYCPQSSRYSTGLKAEKIMKDAVLEAAKKAKEAGSTRFCMGA
 SID20 EIQAVYDPSPLDLLFHGAQ-----SSRYNTGLKAQOKIMNKYAVLEAAKKAKESGSTRFCMGA
 SID22 EIQAVYDPSPLDLLFHGAQVHRNVHKFREVOQCTLLSIKTGCCSEDCSYCPQSSRYNTGLKAQOKIMNKDAVLEAAKKAKESGSTRFCMGA
 SID24 EIQAVYDPSPLDLLFHGAQVHRNVHKFREVOQCTLLSIKTGCCSEDCSYCPQSSRYNTGLKAQOKIMNKYAVLEAAKKAKESGSTRFCMGA
 SID26 EIKSVYDPSPLDLLFHAAQVHRHAHNFREVQCTLLSVKTGCCSEDCSYCPQSSRYDTGVKAQOKIMNKDAVLEQAAEKAKEAGSTRFCMGA
 SID28 QVKSITYDPSPLDLLFHGAQVHRHAHNFREVQCTLLSIKTGCCSEDCSYCPQSSKYDTGVKQGRLMNKAEVLEQAAKKAKEAGSTRFCMGA
 SID32 -----RDAVLEAAKKAKEAGSTRFCMGA
 1705463 EIKSVYDPSPLDLLFHGAQVHRVHNFREVQCTLLSIKTGCCSEDCSYCPQSSRYSTGVKAQRIMSKDAVIDAAKKAKEAGSTRFCMGA
 SID30 EIKAIYDKPLMELCWGAGSLHRKFHPIGAIQMCTLLNIKTGCCSEDCSYCAQSSRYOTGLKASKMWSVESVLAARIAKONGSTRFCMGA
 22995363 EIQKIYDTPPLIDLIFRAASIHRRKFHDPKKVQOCTLLSIKTGGCTEDCKYCAQSSRYNTGVKATKLMKIDEVLEKAKIAKAGSTRFCMGS
 6321725 QLKEIYHTPPLLELTHAAQLOHRKWHDP TKVOLTLMNIKSGGCSEDCKYCAOSSRNDTGLKAEKMKVYDEVILEKAEAKRNGSTRFCIGA

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SID18 SGGIIGLGEAEEDRVGLLHTLATLPTHPESVPINALIAVKGTPLOD-QKP---VEIWMIRMIASARIIVMPKAVRLSAGRVRFMSPE
SID20 SGGIIGLGEAEEDRVGLLHTLATLPTHPESVPINALVAVKGTPLED-QKP---VEIWMIRMILTARITMPKAVRLSAGRVRFMSPE
SID22 SGGIIGLGEAEEDRVGLLHTLATLPTHPESVPINALVAVKGTPLED-QKP---VEIWMIRMILTARITMPKAVRLSAGRVRFMSPE
SID24 SGGIIGLGEAEEDRVGLLHTLATLPTHPESVPINALVAVKGTPLED-QKP---VEIWMIRMILTARITMPKAVRLSAGRVRFMSPE
SID26 SGGIIGLGEAEEDRVGLLHTLATLPTHPESVPINALIAVKGTPLED-QKP---VEIWMIRMILTARIVMPKAVRLSAGRVRFMSPE
SID28 SGGIIGLGEAEEDRVGLLHTLSTLPTHPESVPINALIAVKGTPLED-QKP---VEIWMIRMILTARIVMPKAVRLSAGRVRFMSPE
SID32 SGGIIGLGEAEEDRVGLLHTLATLPTHPESVPINALIAVKGTPLOD-QKP---VEIWMIRMILASARIIVMPKAVRLSAGRVRFMSPE
1705463 SGGIIGLGEAEEDRIGLLHTLATLPTHPESVPINALIAVKGTPLED-QKP---VEIWMIRMIGTARIVMPKAVRLSAGRVRFMSPE
SID30 TGGIIGLGENKSDHIGLLETVATLPSHPESVPVNMVAIKGTPLEG--NKK---VEFENMLRMVATARIVMPKTIIVRLAAGRGELSEOQ
2995363 SGGIIGLGEKKHDRVGLIHSLATMPTHPESVPFNLLVPIPGTPVGDAVKE---LPIHPFLRSIATARICMPKTIIRFAAGRNTCSESE
6321725 TGGIIGLGESEDDHIGFIYTLSNMSPHPESLPINRLVAIKGTPMAEELADPKSKLQFDEILRTIATARIVMPKAIIRLAAGRYTMKETEBE

FIG. 1B



Serial No. 09/740,288
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PLANT BIOTIN SYNTHASE
Filed: 12/19/00

SID18 QALCFLAGANSIFAGEKLLTTANNDFDADQAMFKILGLIPKAP-----NFGDEEATVASTE--RCEQ--AASM
SID20 QALCFLAGANSIFAGEKLLTTANNDFDADQAMFKILGLIPKAP-----SFGEESASAAPTESERSEQ--AASM
SID22 QALCFLAGANSIFAGEKLLTTANNDFDADQAMFKILGLIPKAP-----SFGEESASAAPTESERSEQ--AASM
SID24 QALCFLAGANSIFAGEKLLTTANNDFDADQAMFKILGLIPKAP-----SFGEESASAAPTESERSEQ--AASM
SID26 QALCFLAGANSIFAGEKLLTTANNDFDADQAMFKILGLIPKAP-----NFDQTS-----TSFEAERCEQEATAS-
SID28 QALCFLAGANSIFAGEKLLTTANNDFDADQAMFKILGLIPKAP-----SLHEGE-----TSVTEDY--KEAASSS
SID32 QALCFLAGANSIFAGEKLLTTANNDFDADQAMFKILGLIPKAP-----NFGDEEVMAAPTE--RCEQ--AALM
1705463 QALCFLAGANSIFAGEKLLTTANNDFDADQAMFKILGLIPKAP-----SFSED-----S--ESENCEKVASASH
SID30 QVLCFMAGANAVFTGETMLTTPAVGWGVDSVVFNRWGLRPMESFEVEALKNDKPATTNTEIPEVASKAEMPGTVA
2995363 QALAFMAGANAVFTGEKMLTTPAVSWDSQSOLFYNWGLEGMQSFYGT---STEGEDGTFTLPPKERLAPSPSL
6321725 QFVCFMAGCNSIFTGKMLTTMCNGWDEDKAMLAKWGLQPMFAFKYD-----RS

FIG. 1C

Clone cdt2c.pk002.c17 Contains a 99 Nucleotide Deletion

SID19 CGACTGGAGCCGGCCGAGATCCAGCCGCTCTACGACTCACCGCTCCTCGACCTCCTCTT
SID21 CGACTGGAGCCGGCCGAGATCCAGCCGCTCTACGACTCACCGCTCCTCGACCTCCTCTT
SID19 TCACGGGGGCTCAG-----
SID21 TCACGGGGGCTCAGTCCACAGAAATGTCATAATTCAAGAGAAGTGACGAATGCACACT
SID19 -----TCATCAAG
SID21 TCTTTCAATCAAGACTGGTGATGCAAGTGAAGATTGTTCTTACTGTCTCAGTCAATCAAG
SID19 ATACAACACTGGAATGAAGGCCCAAAAATTGATGAACAATAATGCTGTCTTGAAGCAGC
SID21 ATACAACACTGGAATGAAGGCCCAAAAATTGATGAACAATAATGCTGTCTTGAAGCAGC

FIG. 2